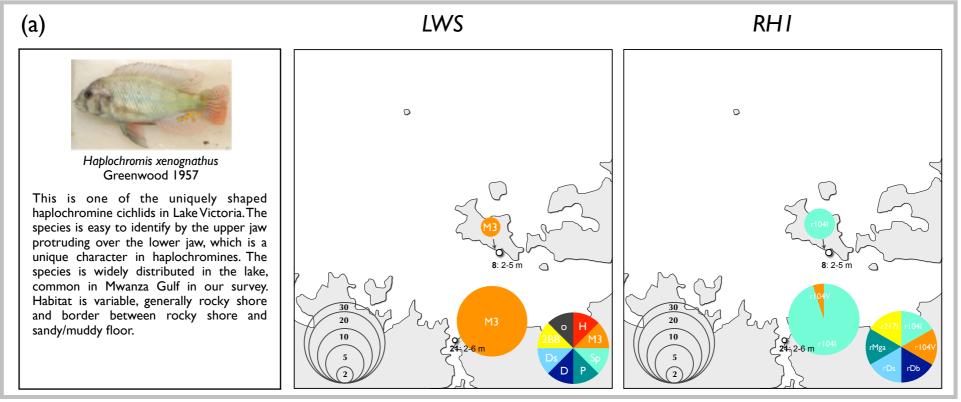
## **Supporting information**



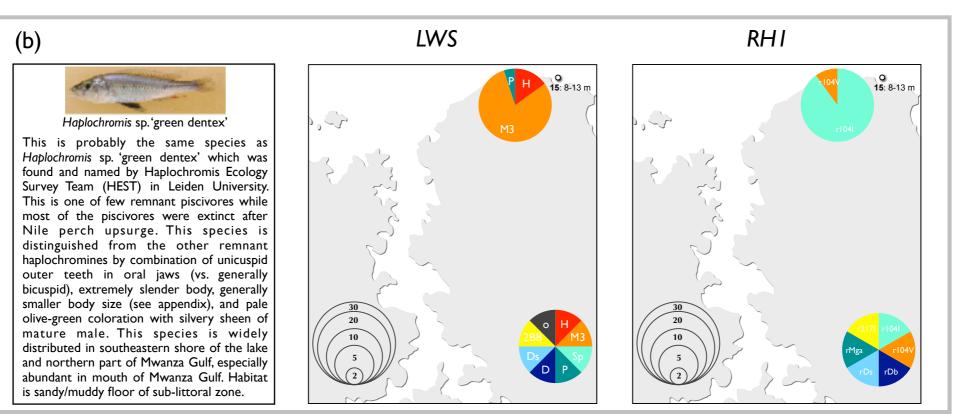
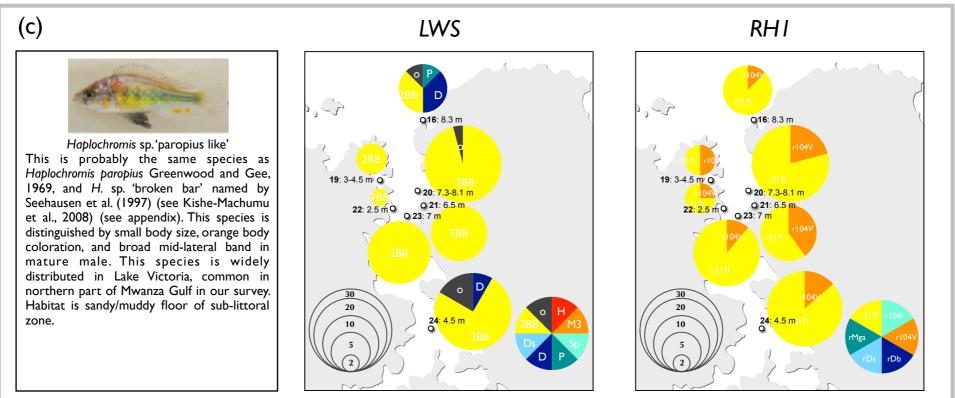


Fig. SI



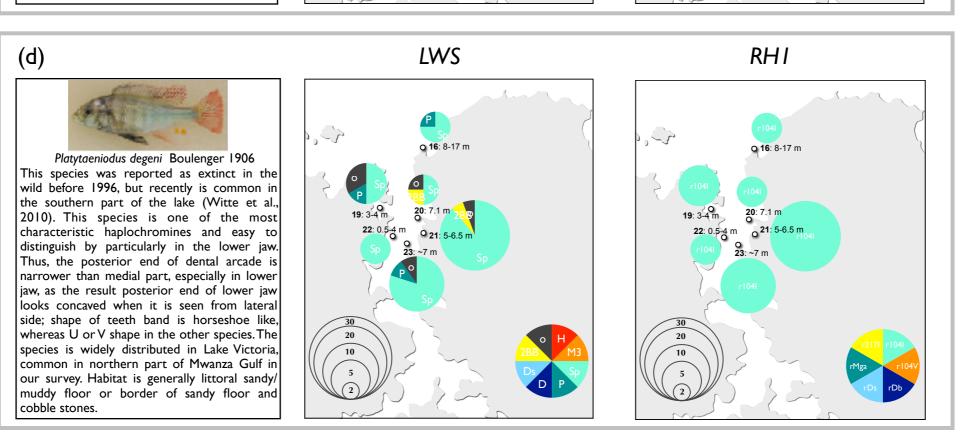
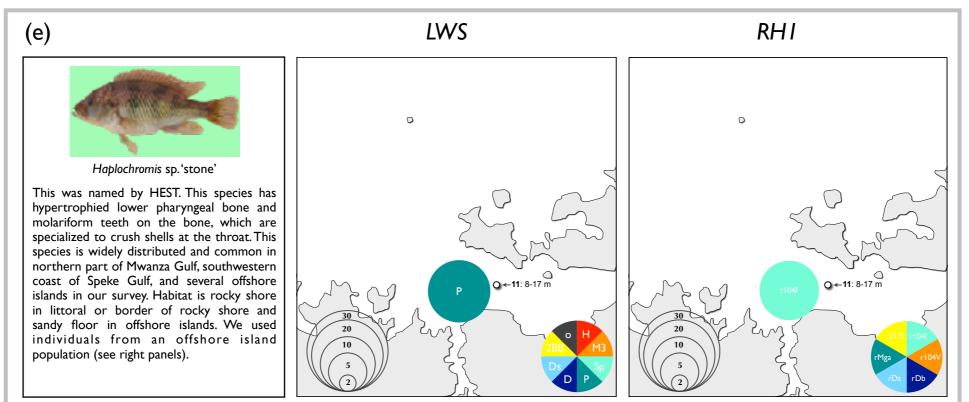


Fig. S1 continued



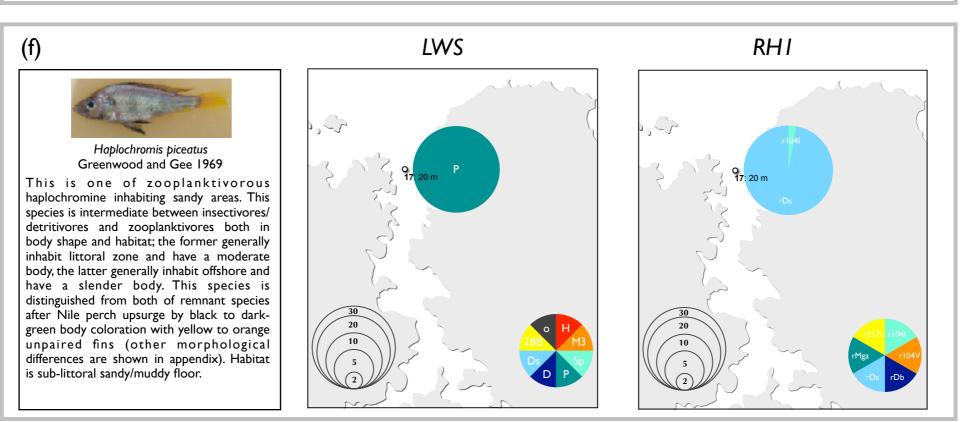
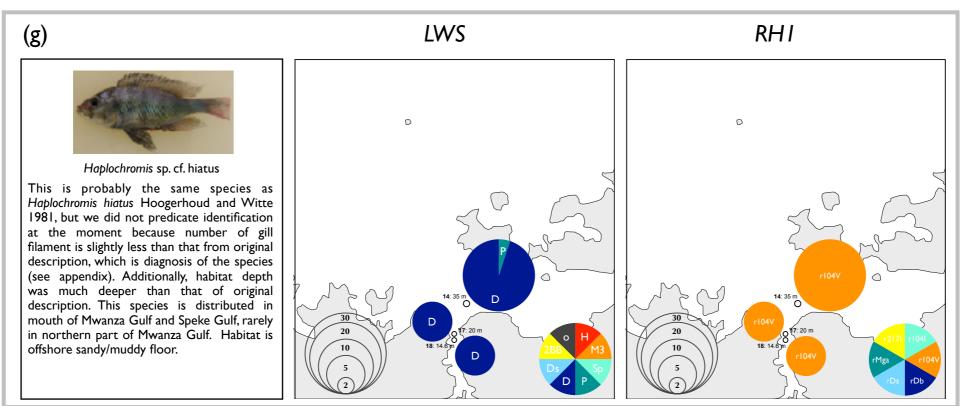


Fig. S1 continued



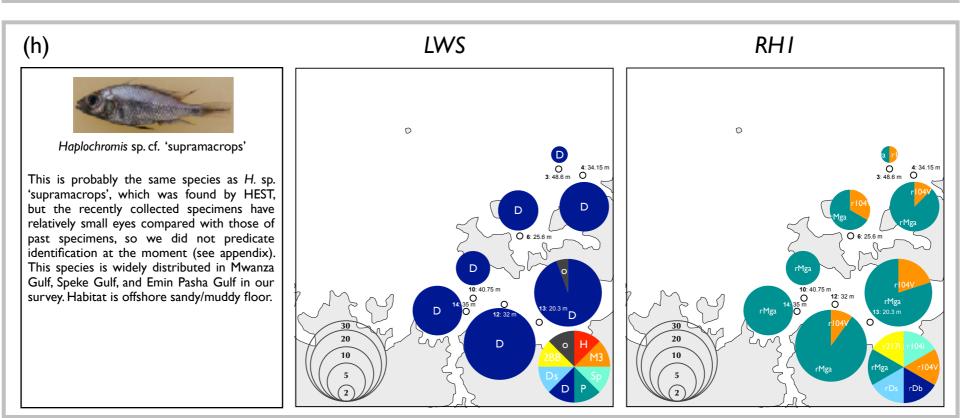
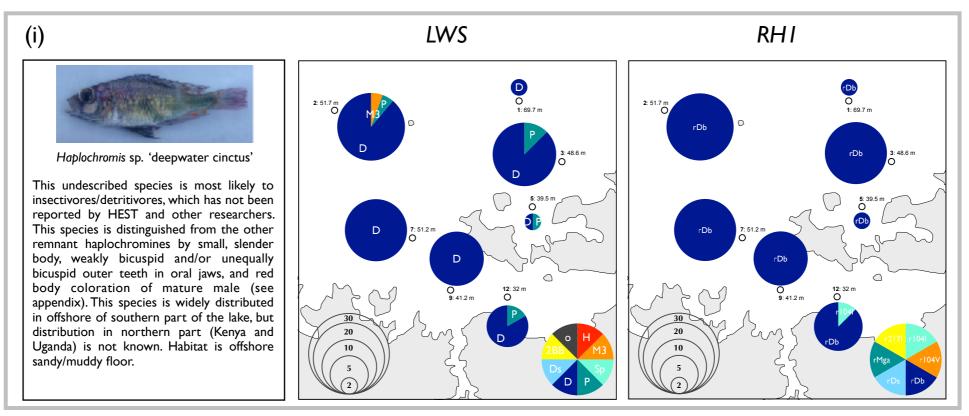


Fig. S1 continued



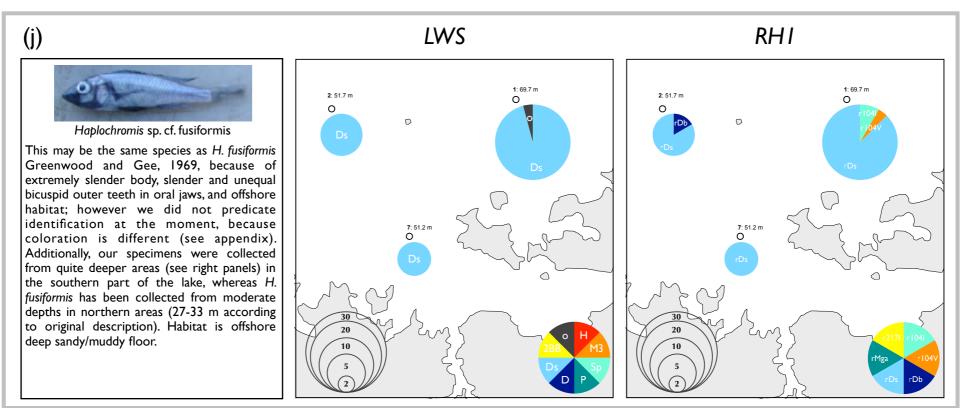


Fig. S1 continued

## Figure S1

Short descriptions of the ten species and the frequencies of *LWS* and *RH1* alleles in the populations of (a) *Haplochromis xenognathus*, (b) *H*. sp. 'green dentex', (c) *H*. sp. 'paropius like', (d) *Platytaeniodus degeni*, (e) *H*. sp. 'stone', (f) *H. piceatus*, (g) *H*. sp. cf. hiatus, (h) *H*. sp. 'supramacrops', (i) *H*. sp. 'deepwater cinctus', and (j) *H*. sp. cf. fusiformis are shown in separate panels. Arabic numerals correspond to those in Fig. 1A, and the depths at each point are described on the right side of the numbers. The size of a pie indicates the number of haplotypes sequenced. The standard sizes of pies are shown at the left bottom. The colored sections of a pie indicate the frequency of the correspondent allele in the standard allele color pie (right bottom). The amino acid differences among allele groups are shown in Fig. 2B (LWS) and 2C (RH1). The maps were drawn by Y. T. based on original source maps: https://www.google.com/maps. Fish photographs were taken by M. I. and S. M.